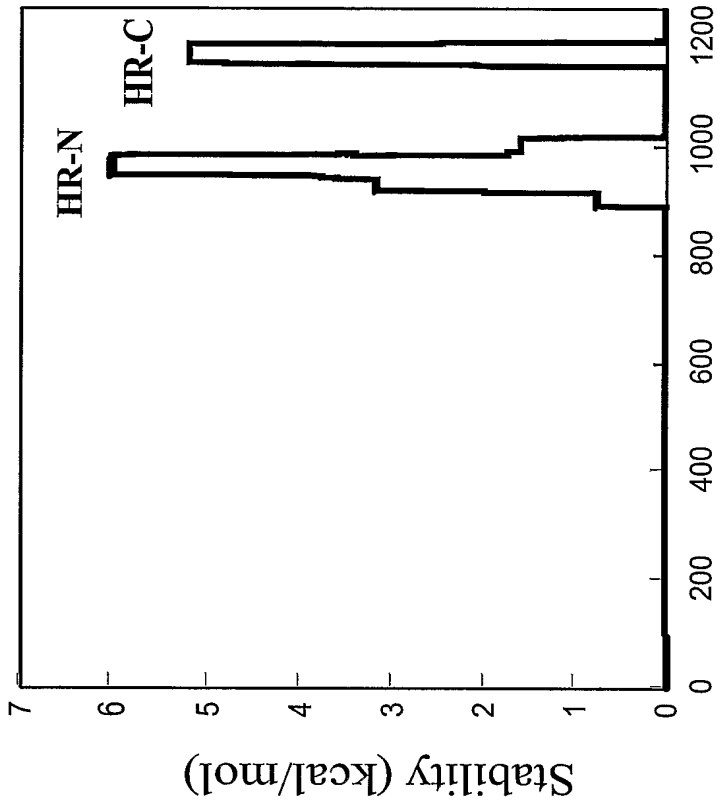
A
HR-N
HR-C
Stability (kcal/mol)
Residue Position
0
1
2
3
4
5
6
7
0
200
400
600
800
1000
1200


B
HR-N
HR-C
Region 1
Region 2
Region 3
851
882
916
927
973
978
1011
1147
1185
1194
1226
1255
Fusion peptide region
Frameshift/ Hinge region
Frameshift/ Hinge region
Transmembrane region

FIG. 1

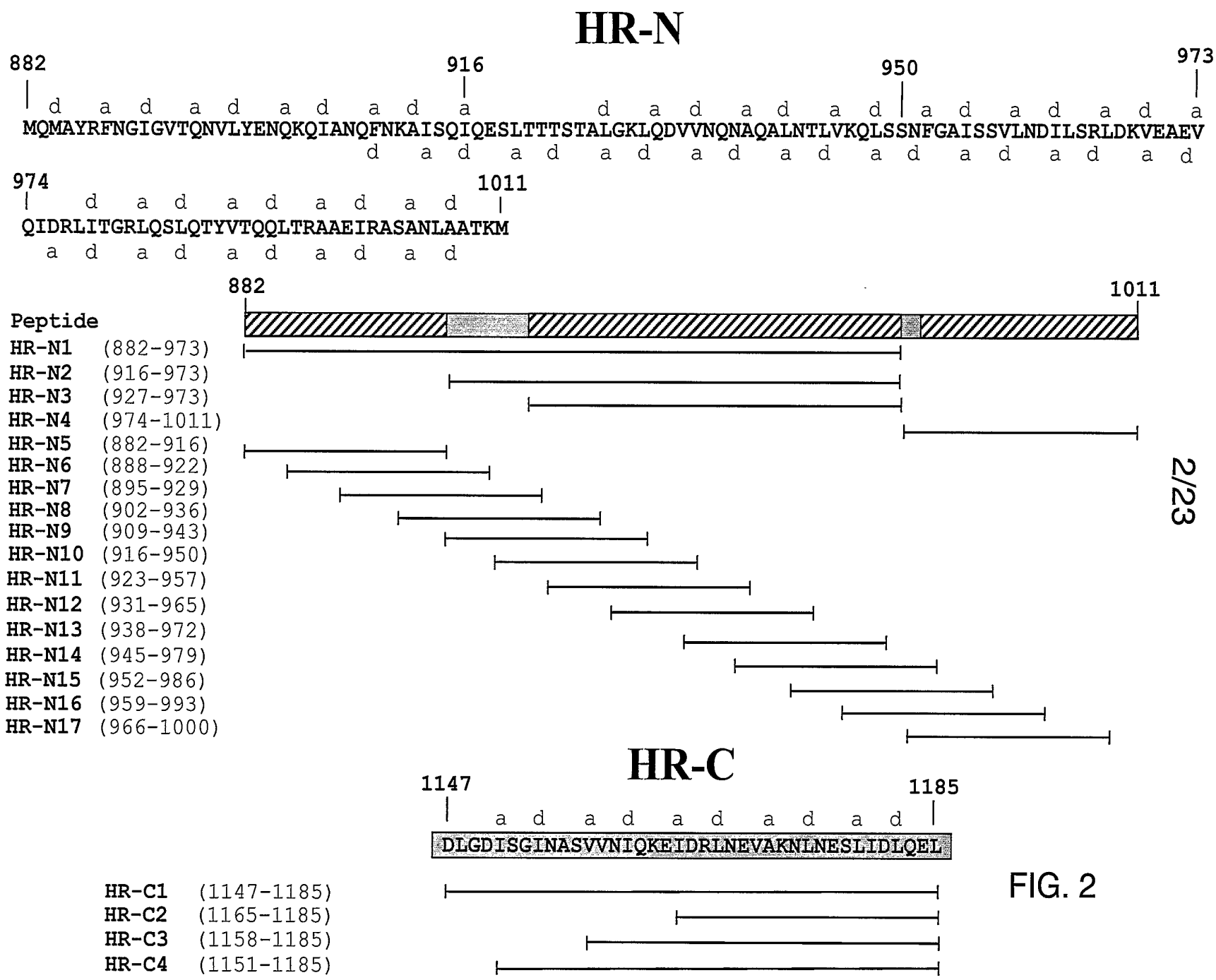
HR-N
882
916
950
973
d a d a d a d a d a d a d a d a d a d a d a d a
MQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEV
d a d a d a d a d a d a d a d a d a d a d
974
1011
d a d a d a d a d
QIDRLITGRLQSLQTYVTQQLTRAAEIRASANLAATKM
a d a d a d a d a d
882
1011
Peptide
HR-N1 (882-973)
HR-N2 (916-973)
HR-N3 (927-973)
HR-N4 (974-1011)
HR-N5 (882-916)
HR-N6 (888-922)
HR-N7 (895-929)
HR-N8 (902-936)
HR-N9 (909-943)
HR-N10 (916-950)
HR-N11 (923-957)
HR-N12 (931-965)
HR-N13 (938-972)
HR-N14 (945-979)
HR-N15 (952-986)
HR-N16 (959-993)
HR-N17 (966-1000)
HR-C
1147
1185
a d a d a d a d a d a d
DLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL
HR-C1 (1147-1185)
HR-C2 (1165-1185)
HR-C3 (1158-1185)
HR-C4 (1151-1185)

FIG. 2

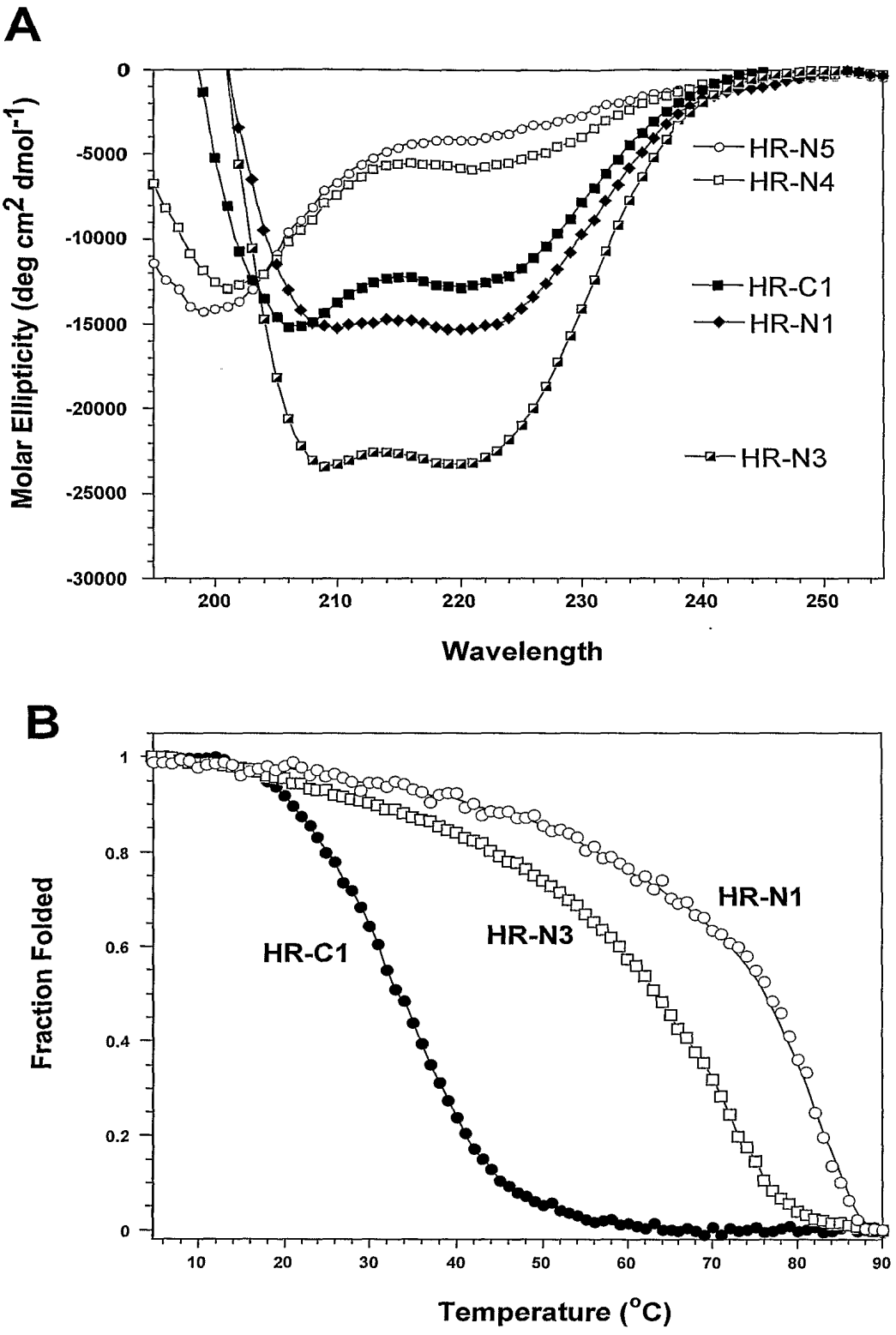
A
Molar Ellipticity (deg cm^2 dmol^{-1})
0
-5000
-10000
-15000
-20000
-25000
-30000
200
210
220
230
240
250
Wavelength
HR-N5
HR-N4
HR-C1
HR-N1
HR-N3
B
Fraction Folded
1
0.8
0.6
0.4
0.2
0
10
20
30
40
50
60
70
80
90
Temperature (°C)
HR-N1
HR-N3
HR-C1

FIG. 3

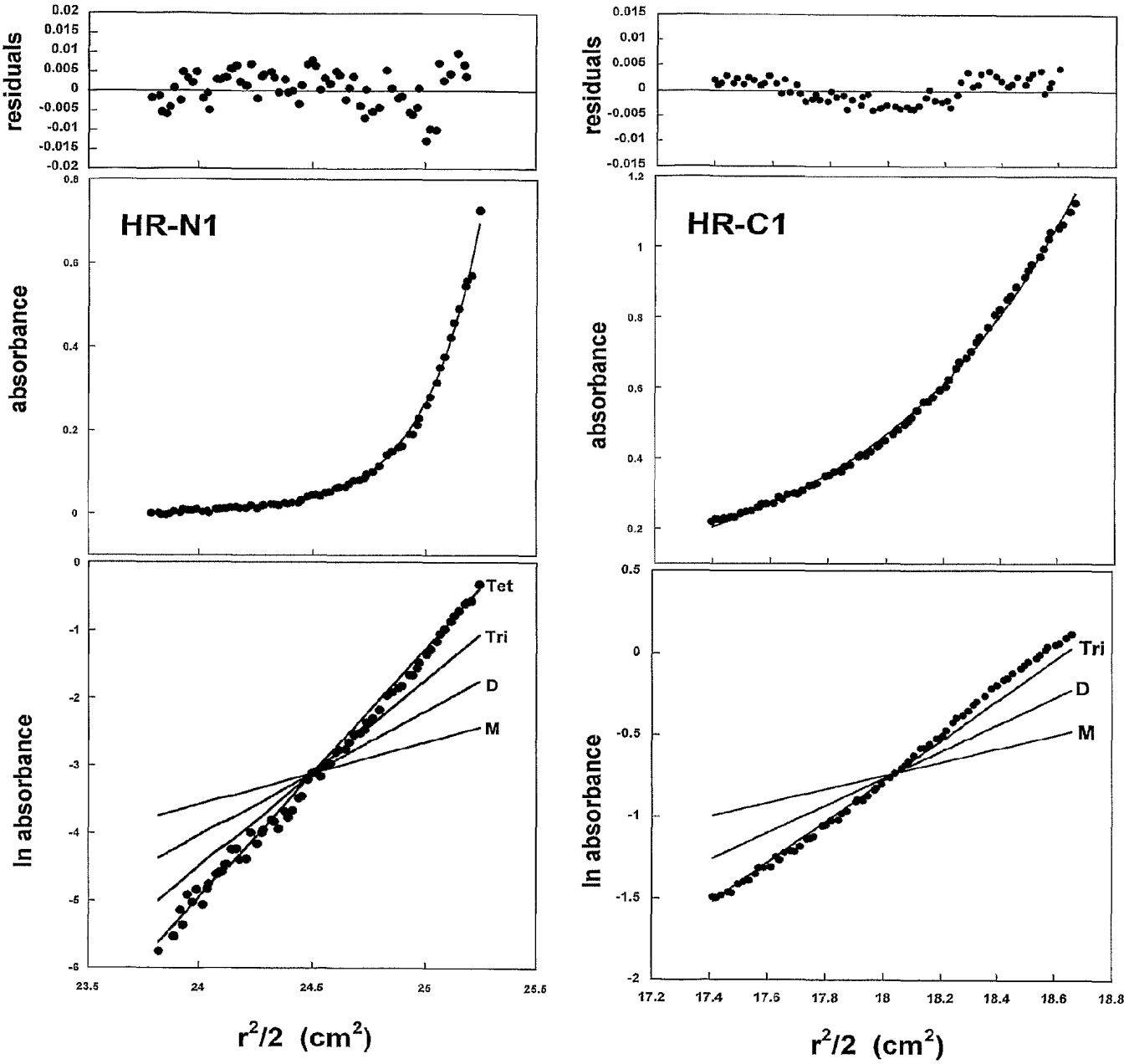
residuals
HR-N1
absorbance
ln absorbance
Tet
Tri
D
M
r²/2 (cm²)
residuals
HR-C1
absorbance
ln absorbance
Tri
D
M
r²/2 (cm²)

FIG. 4

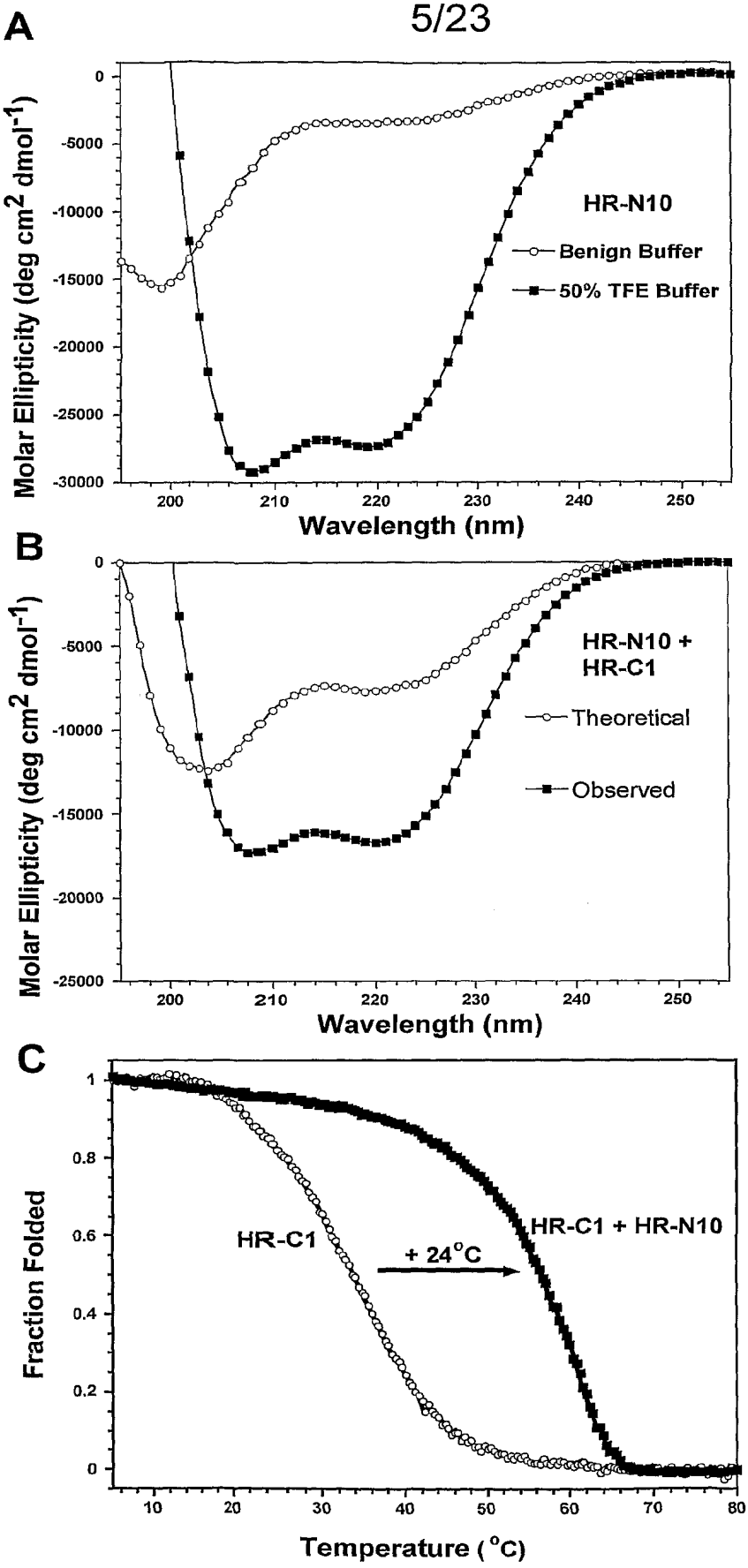
A
Molar Ellipticity (deg cm^2 dmol^{-1})
0
-5000
-10000
-15000
-20000
-25000
-30000
200
210
220
230
240
250
Wavelength (nm)
HR-N10
Benign Buffer
50% TFE Buffer
B
Molar Ellipticity (deg cm^2 dmol^{-1})
0
-5000
-10000
-15000
-20000
-25000
200
210
220
230
240
250
Wavelength (nm)
HR-N10 +
HR-C1
Theoretical
Observed
C
Fraction Folded
1
0.8
0.6
0.4
0.2
0
10
20
30
40
50
60
70
80
Temperature (°C)
HR-C1
+ 24°C
HR-C1 + HR-N10

FIG. 5

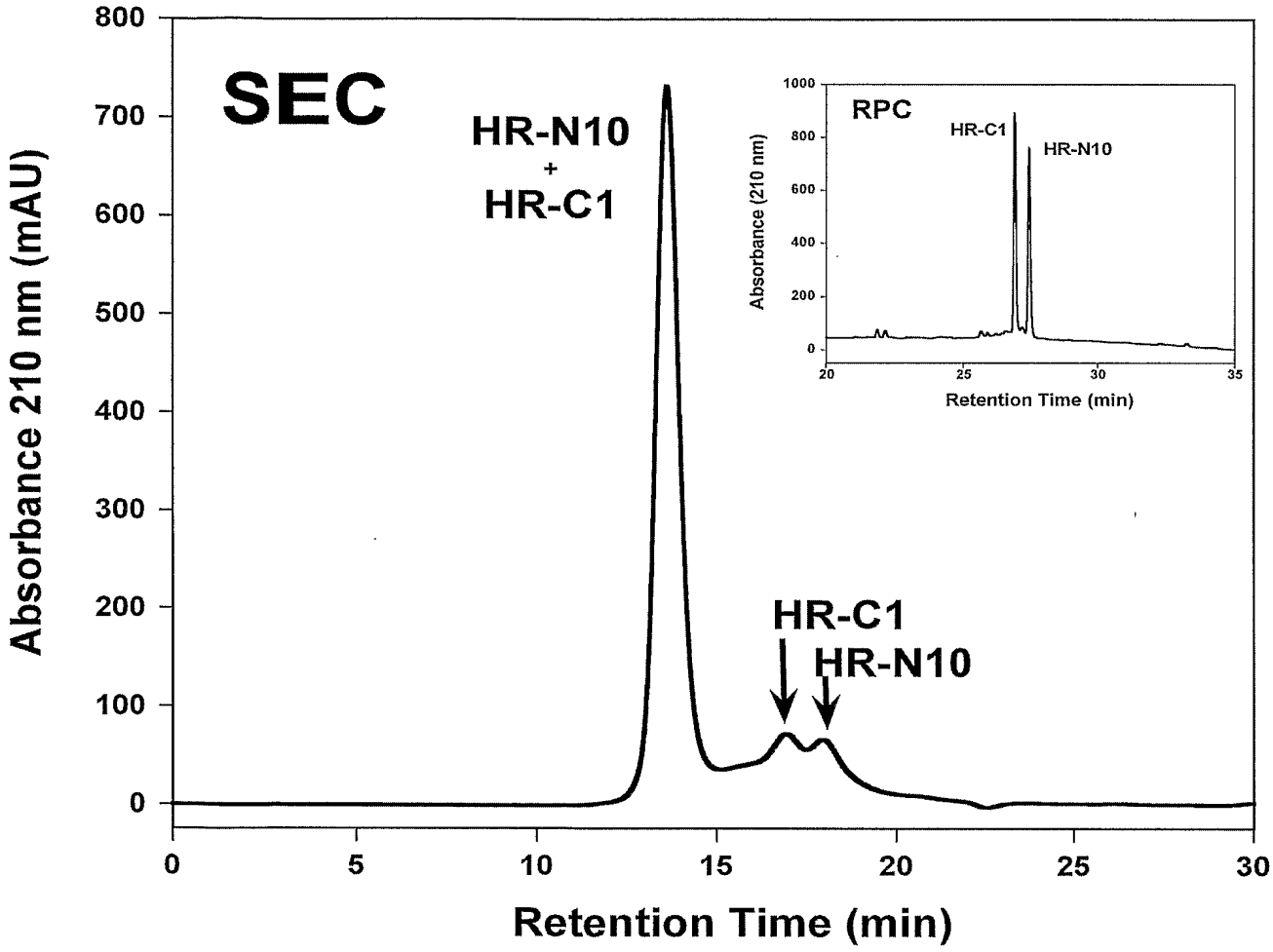
SEC
HR-N10
+
HR-C1
HR-C1
HR-N10
RPC
HR-C1
HR-N10
Absorbance (210 nm)
Retention Time (min)
Absorbance 210 nm (mAU)
Retention Time (min)

FIG. 6

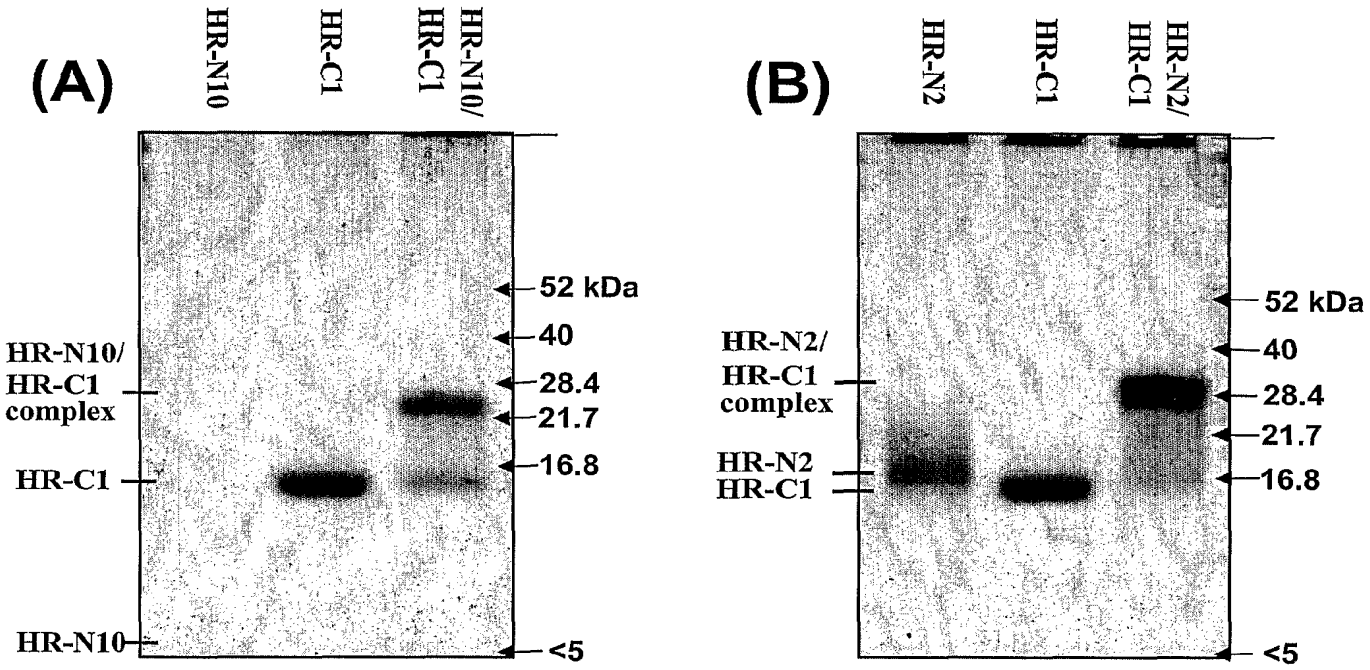
(A)
HR-N10
HR-C1
HR-N10/ HR-C1
52 kDa
40
28.4
21.7
16.8
<5
HR-N10/ HR-C1 complex
HR-C1
HR-N10
(B)
HR-N2
HR-C1
HR-N2/ HR-C1
52 kDa
40
28.4
21.7
16.8
<5
HR-N2/ HR-C1 complex
HR-N2
HR-C1

FIG. 7

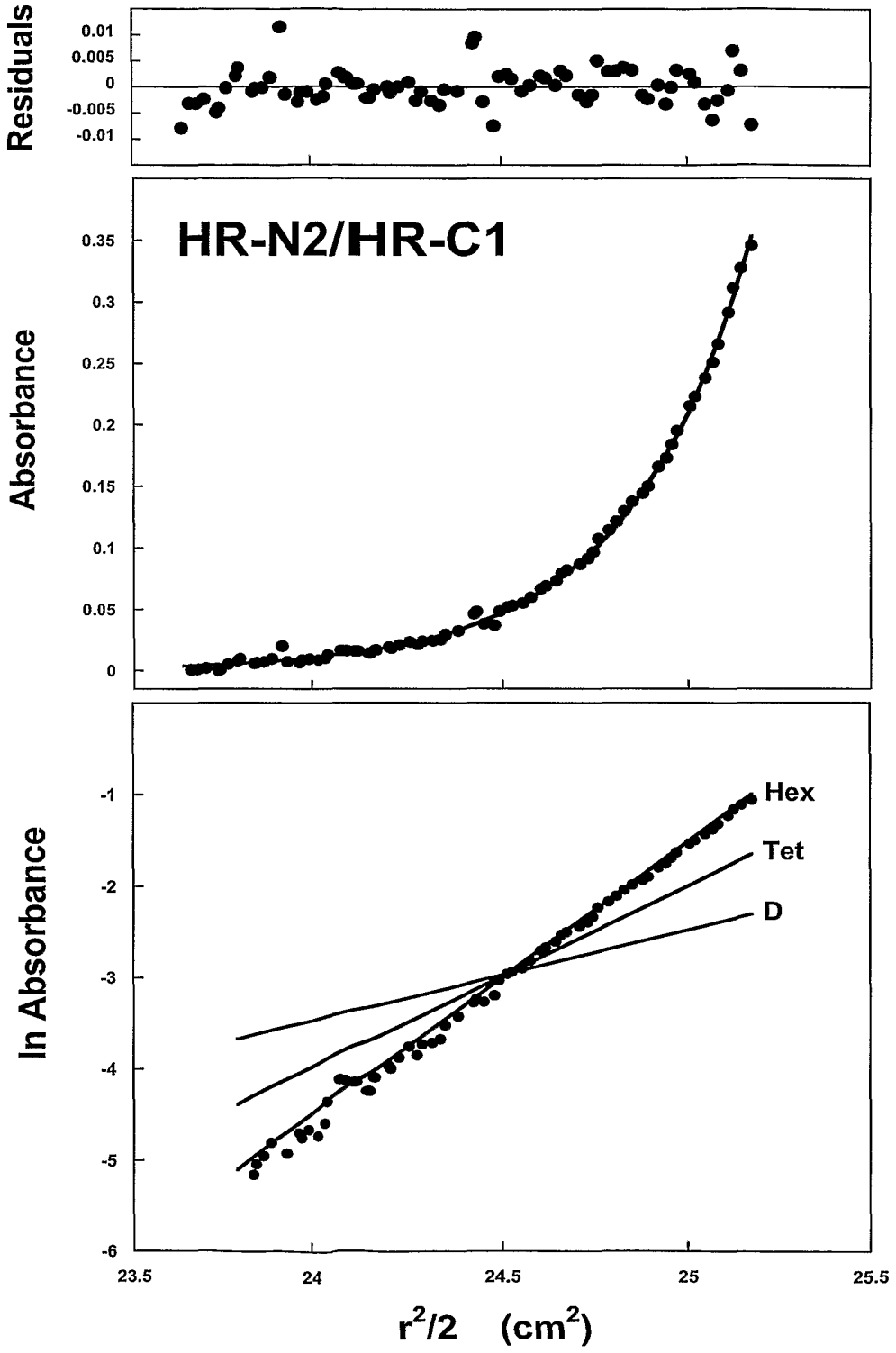
Residuals
0.01
0.005
0
-0.005
-0.01
HR-N2/HR-C1
Absorbance
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
ln Absorbance
-1
-2
-3
-4
-5
-6
Hex
Tet
D
23.5
24
24.5
25
25.5
r²/2 (cm²)

FIG. 8

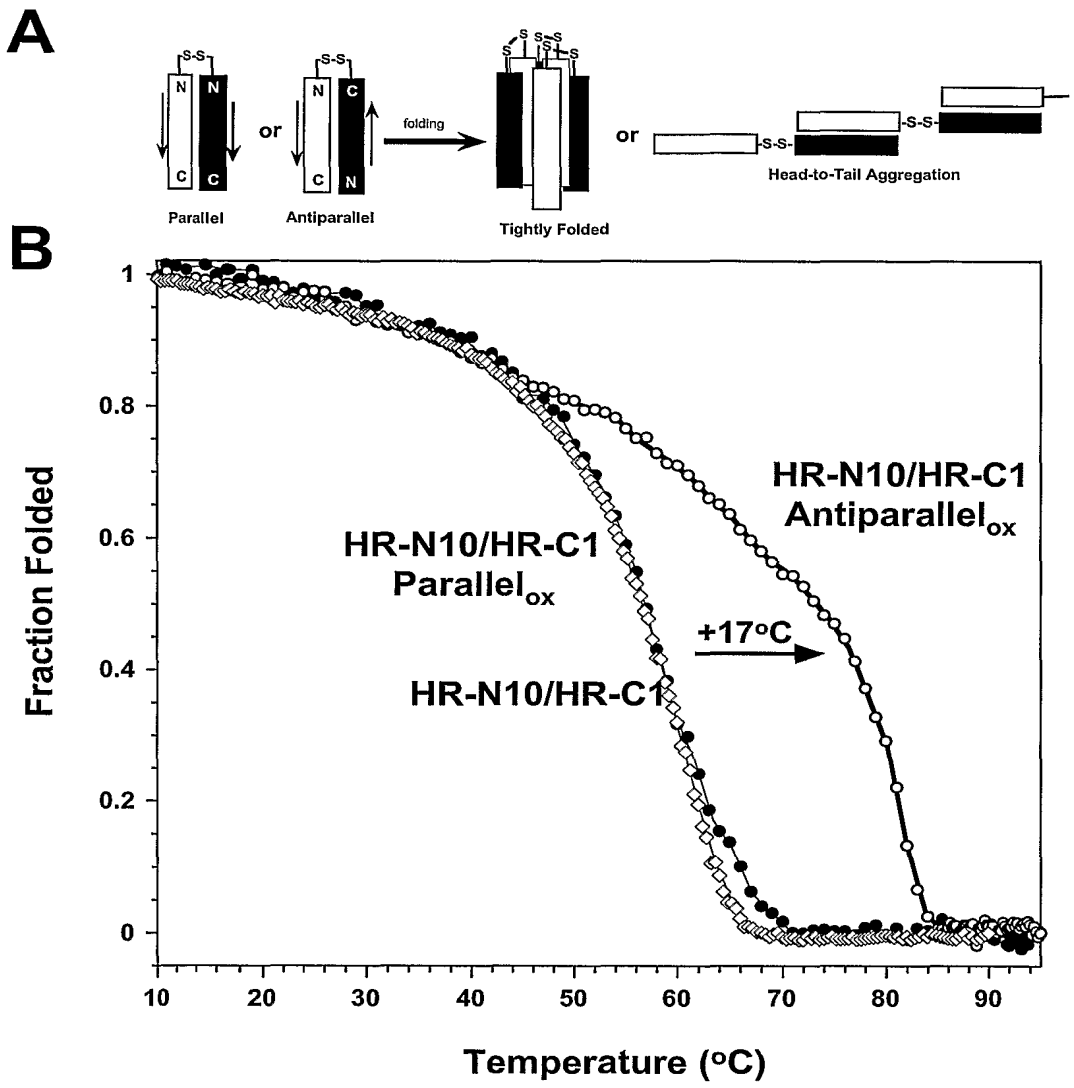
A
S-S
N
C
or
folding
Parallel
Antiparallel
Tightly Folded
Head-to-Tail Aggregation
B
Fraction Folded
1
0.8
0.6
0.4
0.2
0
10
20
30
40
50
60
70
80
90
Temperature (°C)
HR-N10/HR-C1
Antiparallel$_{ox}$
HR-N10/HR-C1
Parallel$_{ox}$
+17°C
HR-N10/HR-C1

FIG. 9

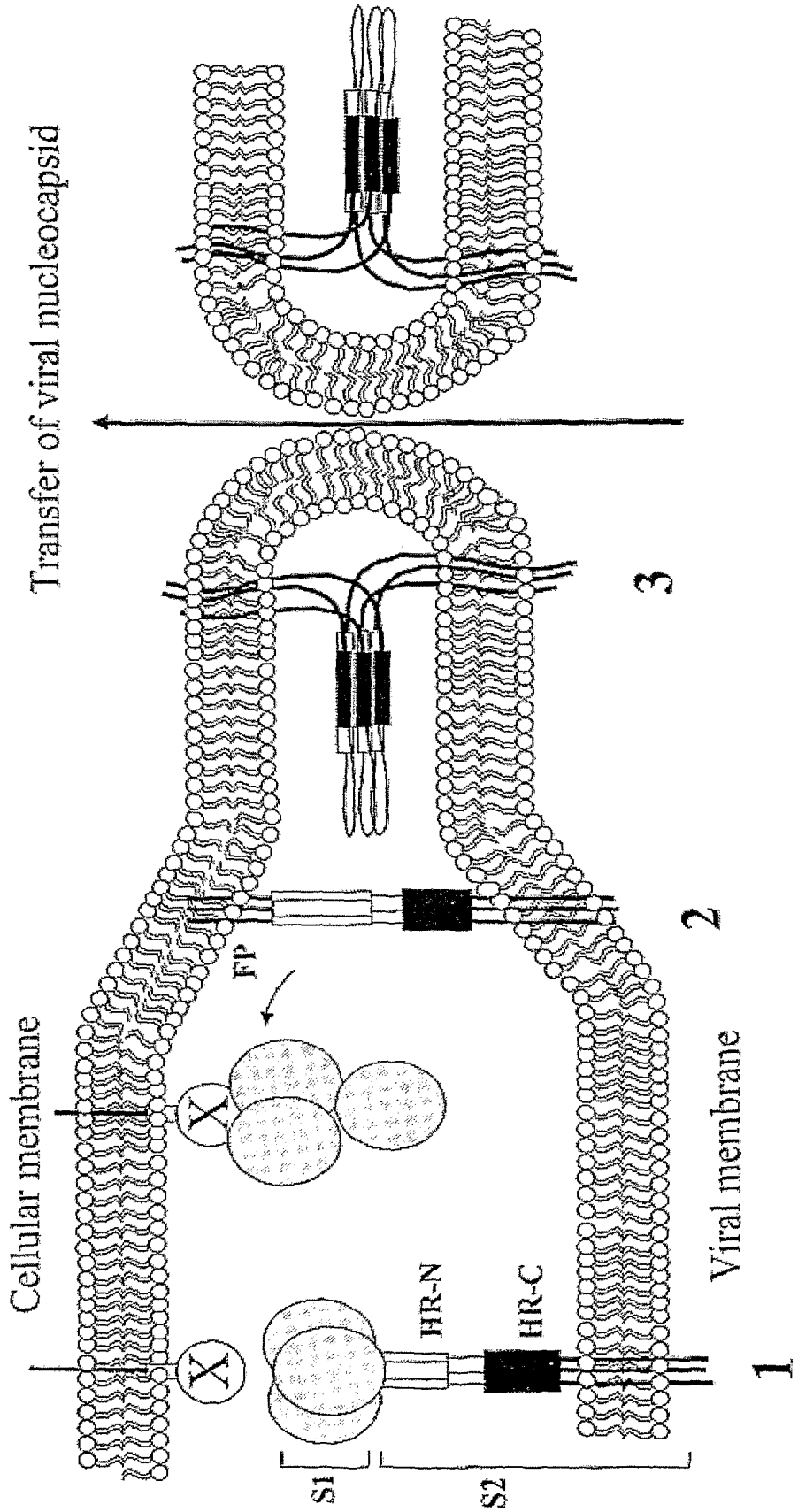
Transfer of viral nucleocapsid
3
2
1
FP
HR-N
HR-C
S1
S2
Cellular membrane
Viral membrane

FIG. 10

HR-N (916-950)

(native)

Ac-IQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS-amide

(Ala, Lys and Arg substituted)

Ac-IQAALTKTSAALGKLQAAVNRNAAALNKLVKALSS-amide

(Aib=B substituted)

Ac-IQESLTBTSTALGKLQDVVNBNAQALNBLVKQLSS-amide

(Dxg=Z substituted)

Ac-IQESLTZTSTALGKLQDVVNZNAQALNZLVKQLSS-amide

HR-C (1151-1185)

(native)

Ac-ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL-amide

(Ala, Lys and Arg substituted)

Ac-IAAINKSVAAIQKEIARLNEVAKALNASLIRLQAL-amide

(Aib=B substituted)

Ac-ISGINBSVVNIQKEIDRLNBVAKNLNBSLIDLQEL-amide

(Dxg=Z substituted)

Ac-ISGINZSVVNIQKEIDRLNZVAKNLNZSLIDLQEL-amide

FIG. 11

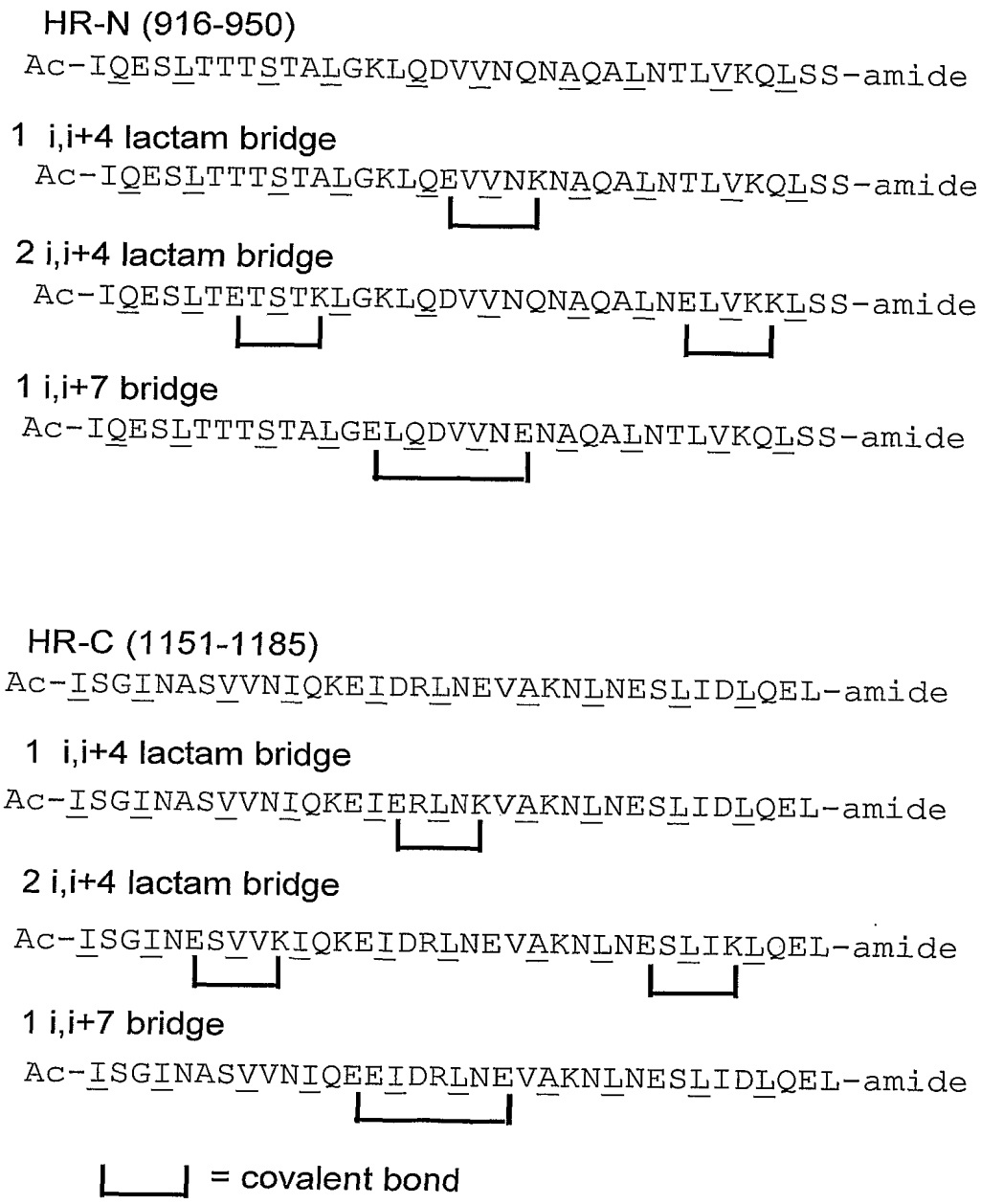
HR-N (916-950)
Ac-IQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS-amide
1 i,i+4 lactam bridge
Ac-IQESLTTTSTALGKLQEVVNKNAQALNTLVKQLSS-amide
2 i,i+4 lactam bridge
Ac-IQESLTETSTKLGKLQDVVNQNAQALNELVKKLSS-amide
1 i,i+7 bridge
Ac-IQESLTTTSTALGELQDVVNENAQALNTLVKQLSS-amide
HR-C (1151-1185)
Ac-ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL-amide
1 i,i+4 lactam bridge
Ac-ISGINASVVNIQKEIERLNKVAKNLNESLIDLQEL-amide
2 i,i+4 lactam bridge
Ac-ISGINESVVKIQKEIDRLNEVAKNLNESLIKLQEL-amide
1 i,i+7 bridge
Ac-ISGINASVVNIQEEIDRLNEVAKNLNESLIDLQEL-amide
= covalent bond

FIG. 12

HR-N (916-950)

Ac-IQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSS-amide

(Ile and Leu substituted into the hydrophobic core)

Ac-I**I**ESLTTT**I**TALGKL**I**DV**L**NQN**I**QALNTL**I**KQLSS-amide

HR-C (1151-1185)

Ac-ISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL-amide

(Ile substituted into the hydrophobic core)

Ac-ISGINAS**I**VNIQKEIDRLNEV**I**KNLNESLIDLQEL-amide

FIG. 13

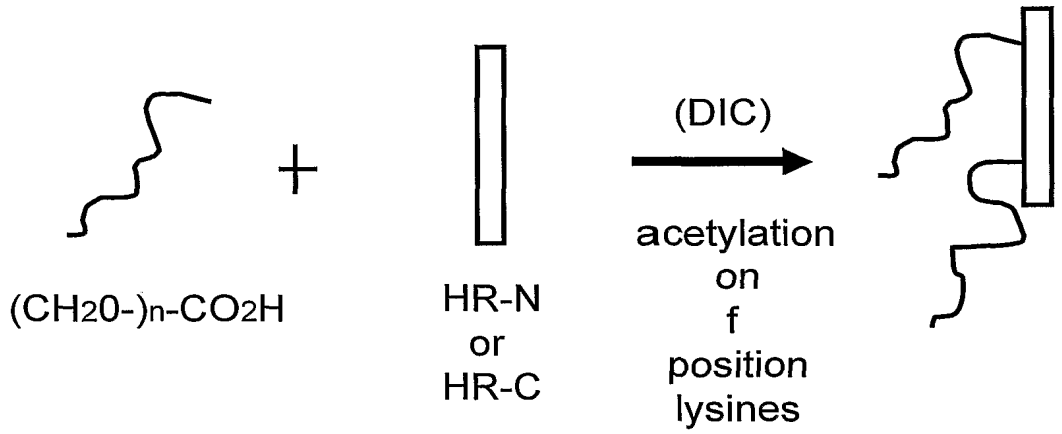

FIG. 14

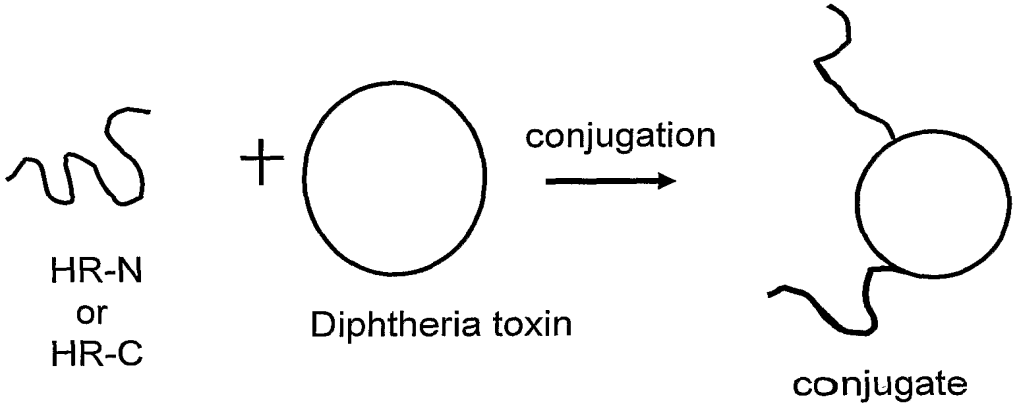

FIG. 15

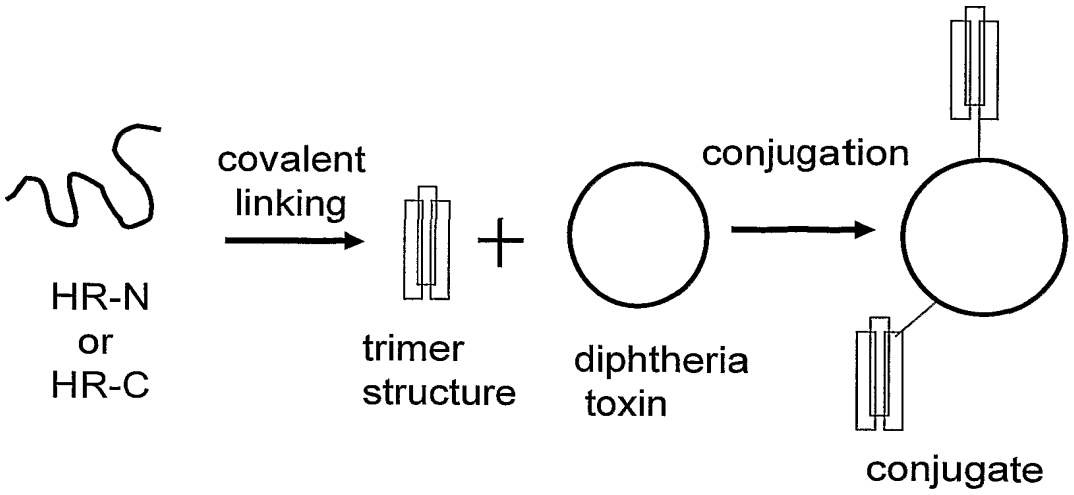

FIG. 16A

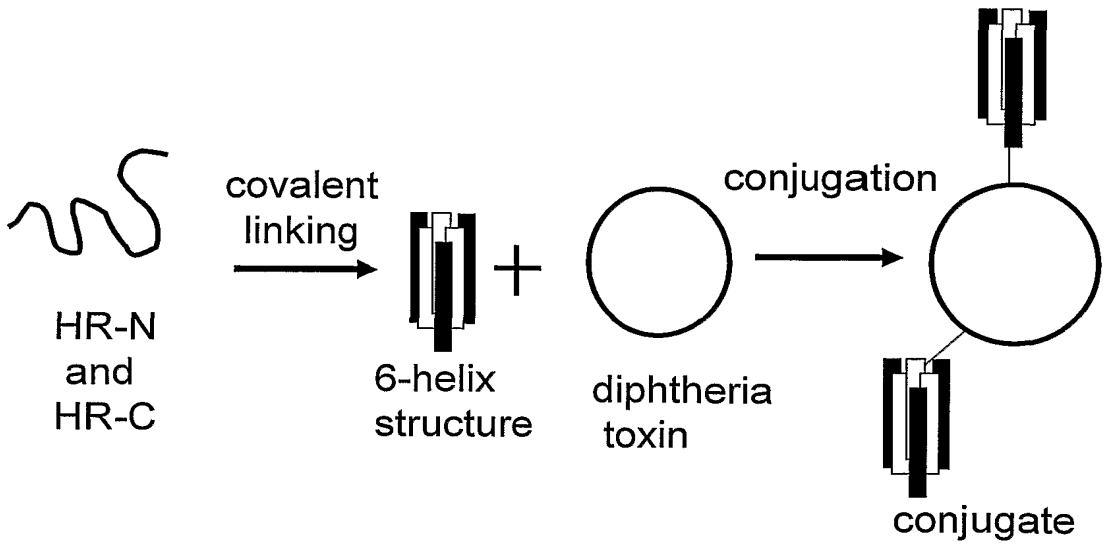

FIG. 16B

A

Coiled-coil template

BB-nLGCAAL***I**L***I**L***I**L***IRRRRNH2
Ac-CAAL***I**L***I**L***I**L***IRRRRNH2

HR-N and HR-C sequences incorporated into the template

HR-N(920-945)	CAALTTTITALGKLIDVLNQNIQALNTLIRRRR-amide
HR-C(1161-1186)	CAALQKEIDRLNEVIKNLNESIIDLQELIRRRR-amide

B

General outline of the experimental procedures used to prepare the template-carrier protein conjugates for immunization

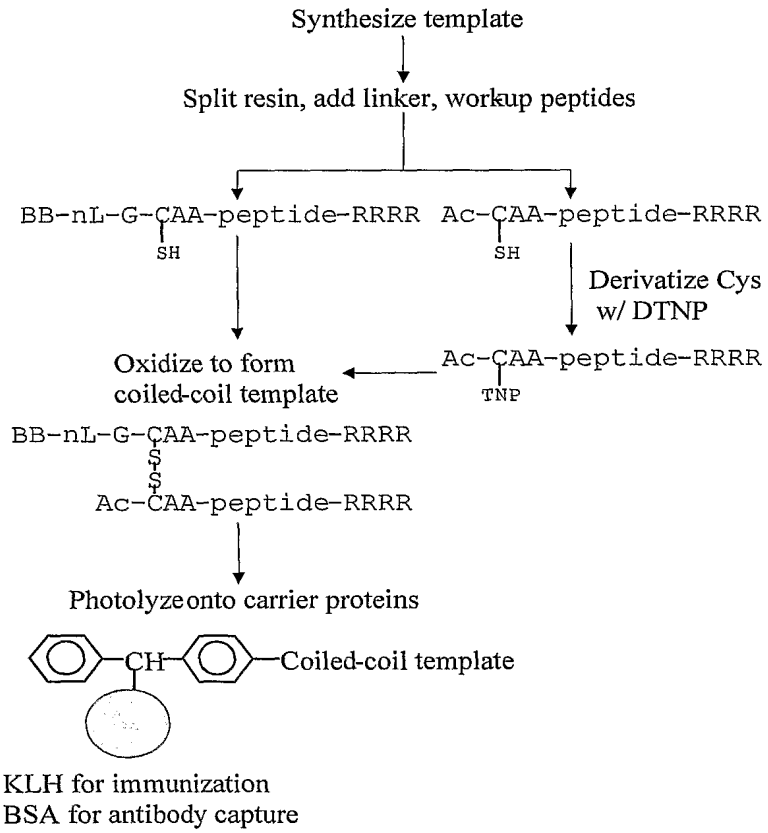

FIG. 17

HR-N peptides, HR-N1 to HR-N17.

Nucleotide sequences for SARS peptides. The amino acid region is shown in brackets.

HR-N1 (882-973)
ATGCAAATGGCATATAGGTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCA
AAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATTCAAGAATCACTTACAACAA
CATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTAAACACA
CTTGTTAAACAACTTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTAAATGATATCCTTTC
GCGACTTGATAAAGTCGAGGCGGAGGTA

HR-N2 (916-973)
ATTCAAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCA
GAATGCTCAAGCATTAAACACACTTGTTAAACAACTTAGCTCTAATTTTGGTGCAATTTCAA
GTGTGCTAAATGATATCCTTTCGCGACTTGATAAAGTCGAGGCGGAGGTA

HR-N3 (927-973)
TTGGGCAAGCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTAAACACACTTGTTAAACA
ACTTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTAAATGATATCCTTTCGCGACTTGATA
AAGTCGAGGCGGAGGTA

HR-N4 (974-1011)
CAAATTGACAGGTTAATTACAGGCAGACTTCAAAGCCTTCAAACCTATGTAACACAACAACT
AATCAGGGCTGCTGAAATCAGGGCTTCTGCTAATCTTGCTGCTACTAAAATG

HR-N5 (882-916)
ATGCAAATGGCATATAGGTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCA
AAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATT

HR-N6 (888-922)
TTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCAAAAACAAATCGCCAACCA
ATTTAACAAGGCGATTAGTCAAATTCAAGAATCACTTACAACA

HR-N7 (895-929)
CAAAATGTTCTCTATGAGAACCAAAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCA
AATTCAAGAATCACTTACAACAACATCAACTGCATTGGGCAAG

FIG. 18A

HR-N8 (902-936)
CAAAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATTCAAGAATCACTTACAAC
AACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAG

HR-N9 (909-943)
TTTAACAAGGCGATTAGTCAAATTCAAGAATCACTTACAACAACATCAACTGCATTGGGCAA
GCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTAAACACA

HR-N10 (916-950)
ATTCAAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCA
GAATGCTCAAGCATTAAACACACTTGTTAAACAACTTAGCTCT

HR-N11 (923-957)
ACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTAAACAC
ACTTGTTAAACAACTTAGCTCTAATTTTGGTGCAATTTCAAGT

HR-N12 (931-965)
CAAGACGTTGTTAACCAGAATGCTCAAGCATTAAACACACTTGTTAAACAACTTAGCTCTAA
TTTTGGTGCAATTTCAAGTGTGCTAAATGATATCCTTTCGCGA

HR-N13 (938-972)
GCTCAAGCATTAAACACACTTGTTAAACAACTTAGCTCTAATTTTGGTGCAATTTCAAGTGT
GCTAAATGATATCCTTTCGCGACTTGATAAAGTCGAGGCGGAG

HR-N14 (945-979)
GTTAAACAACTTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTAAATGATATCCTTTCGCG
ACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATT

HR-N15 (952-986)
TTTGGTGCAATTTCAAGTGTGCTAAATGATATCCTTTCGCGACTTGATAAAGTCGAGGCGGA
GGTACAAATTGACAGGTTAATTACAGGCAGACTTCAAAGCCTT

HR-N16 (959-993)
CTAAATGATATCCTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAAT
TACAGGCAGACTTCAAAGCCTTCAAACCTATGTAACACAACAA

HR-N17 (966-1000)
CTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATTACAGGCAGACTTCAAAGCCT
TCAAACCTATGTAACACAACAACTAATCAGGGCTGCTGAAATC

FIG. 18B

HR-C peptides, HR-C1 to HR-C4

Nucleotide sequences for SARS peptides. The amino acid region is shown in brackets.

HR-C1 (1147-1185)
GATGTTGATCTTGGCGACATTTCAGGCATTAACGCTTCTGTCGTCAACATTCAAAAAGAAAT
TGACCGCCTCAATGAGGTCGCTAAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTG

HR-C2 (1165-1185)
ATTGACCGCCTCAATGAGGTCGCTAAAAATTTAAATGAATCACTCATTGACCTTCAAGAATT
G

HR-C3 (1158-1185)
GTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGAGGTCGCTAAAAATTTAAATGAATC
ACTCATTGACCTTCAAGAATTG

HR-C4 (1151-1185)
ATTTCAGGCATTAACGCTTCTGTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGAGGT
CGCTAAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTG

Amino acid sequence for SARS peptide HR-C1

HR-C1 (1147-1185)
DLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL

FIG. 19

HR-N

Nucleotide sequences for SARS peptides. The amino acid region is shown in brackets.

HR-N (882-1011)

ATGCAAATGGCATATAGGTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAG
AACCAAAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATTCAAGAATCACTTAC
AACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGAATGCTCAAGCATTAA
ACACACTTGTTAAACAACTTAGCTCTAATTTTGGTGCAATTTCAAGTGTGCTAAATGATATC
CTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATTACAGGCAGACT
TCAAAGCCTTCAAACCTATGTAACACAACAACTAATCAGGGCTGCTGAAATCAGGGCTTCTG
CTAATCTTGCTGCTACTAAAATG

FIG. 20

ATGTTTATTTTCTTATTATTTCTTACTCTCACTAGTGGTAGTGACCTTGACCGGTGCACCACTTTTGATG
ATGTTCAAGCTCCTAATTACACTCAACATACTTCATCTATGAGGGGGGTTTACTATCCTGATGAAATTTT
TAGATCAGACACTCTTTATTTAACTCAGGATTTATTTCTTCCATTTTATTCTAATGTTACAGGGTTTCAT
ACTATTAATCATACGTTTGGCAACCCTGTCATACCTTTTAAGGATGGTATTTATTTTGCTGCCACAGAGA
AATCAAATGTTGTCCGTGGTTGGGTTTTTGGTTCTACCATGAACAACAAGTCACAGTCGGTGATTATTAT
TAACAATTCTACTAATGTTGTTATACGAGCATGTAACTTTGAATTGTGTGACAACCCTTTCTTTGCTGTT
TCTAAACCCATGGGTACACAGACACATACTATGATATTCGATAATGCATTTAATTGCACTTTCGAGTACA
TATCTGATGCCTTTTCGCTTGATGTTTCAGAAAAGTCAGGTAATTTTAAACACTTACGAGAGTTTGTGTT
TAAAAATAAAGATGGGTTTCTCTATGTTTATAAGGGCTATCAACCTATAGATGTAGTTCGTGATCTACCT
TCTGGTTTTAACACTTTGAAACCTATTTTTAAGTTGCCTCTTGGTATTAACATTACAAATTTTAGAGCCA
TTCTTACAGCCTTTTCACCTGCTCAAGACATTTGGGGCACGTCAGCTGCAGCCTATTTTGTTGGCTATTT
AAAGCCAACTACATTTATGCTCAAGTATGATGAAAATGGTACAATCACAGATGCTGTTGATTGTTCTCAA
AATCCACTTGCTGAACTCAAATGCTCTGTTAAGAGCTTTGAGATTGACAAAGGAATTTACCAGACCTCTA
ATTTCAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCCCTAATATTACAAACTTGTGTCCTTTTGGAGA
GGTTTTTAATGCTACTAAATTCCCTTCTGTCTATGCATGGGAGAGAAAAAAAATTTCTAATTGTGTTGCT
GATTACTCTGTGCTCTACAACTCAACATTTTTTTCAACCTTTAAGTGCTATGGCGTTTCTGCCACTAAGT
TGAATGATCTTTGCTTCTCCAATGTCTATGCAGATTCTTTTGTAGTCAAGGGAGATGATGTAAGACAAAT
AGCGCCAGGACAAACTGGTGTTATTGCTGATTATAATTATAAATTGCCAGATGATTTCATGGGTTGTGTC
CTTGCTTGGAATACTAGGAACATTGATGCTACTTCAACTGGTAATTATAATTATAAATATAGGTATCTTA
GACATGGCAAGCTTAGGCCCTTTGAGAGAGACATATCTAATGTGCCTTTCTCCCCTGATGGCAAACCTTG
CACCCCACCTGCTCTTAATTGTTATTGGCCATTAAATGATTATGGTTTTTACACCACTACTGGCATTGGC
TACCAACCTTACAGAGTTGTAGTACTTTCTTTTGAACTTTTAAATGCACCGGCCACGGTTTGTGGACCAA
AATTATCCACTGACCTTATTAAGAACCAGTGTGTCAATTTTAATTTTAATGGACTCACTGGTACTGGTGT
GTTAACTCCTTCTTCAAAGAGATTTCAACCATTTCAACAATTTGGCCGTGATGTTTCTGATTTCACTGAT
TCCGTTCGAGATCCTAAAACATCTGAAATATTAGACATTTCACCTTGCTCTTTTGGGGGTGTAAGTGTAA
TTACACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTCTATATCAAGATGTTAACTGCACTGATGTTTC
TACAGCAATTCATGCAGATCAACTCACACCAGCTTGGCGCATATATTCTACTGGAAACAATGTATTCCAG
ACTCAAGCAGGCTGTCTTATAGGAGCTGAGCATGTCGACACTTCTTATGAGTGCGACATTCCTATTGGAG
CTGGCATTTGTGCTAGTTACCATACAGTTTCTTTATTACGTAGTACTAGCCAAAAATCTATTGTGGCTTA
TACTATGTCTTTAGGTGCTGATAGTTCAATTGCTTACTCTAATAACACCATTGCTATACCTACTAACTTT
TCAATTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCTCCGTAGATTGTAATATGTACA
TCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCCAATATGGTAGCTTTTGCACACAACTAAATCG
TGCACTCTCAGGTATTGCTGCTGAACAGGATCGCAACACACGTGAAGTGTTCGCTCAAGTCAAACAAATG
TACAAAACCCCAACTTTGAAATATTTTGGTGGTTTTAATTTTTCACAAATATTACCTGACCCTCTAAAGC
CAACTAAGAGGTCTTTTATTGAGGACTTGCTCTTTAATAAGGTGACACTCGCTGATGCTGGCTTCATGAA
GCAATATGGCGAATGCCTAGGTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGTTCAATGGACTT
ACAGTGTTGCCACCTCTGCTCACTGATGATATGATTGCTGCCTACACTGCTGCTCTAGTTAGTGGTACTG
CCACTGCTGGATGGACATTTGGTGCTGGCGCTGCTCTTCAAATACCTTTTGCTATGCAAATGGCATATAG
GTTCAATGGCATTGGAGTTACCCAAAATGTTCTCTATGAGAACCAAAAACAAATCGCCAACCAATTTAAC
AAGGCGATTAGTCAAATTCAAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTG
TTAACCAGAATGCTCAAGCATTAAACACACTTGTTAAACAACTTAGCTCTAATTTTGGTGCAATTTCAAG
TGTGCTAAATGATATCCTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACAGGTTAATTACA
GGCAGACTTCAAAGCCTTCAAACCTATGTAACACAACAACTAATCAGGGCTGCTGAAATCAGGGCTTCTG
CTAATCTTGCTGCTACTAAAATGTCTGAGTGTGTTCTTGGACAATCAAAAAGAGTTGACTTTTGTGGAAA
GGGCTACCACCTTATGTCCTTCCCACAAGCAGCCCCGCATGGTGTTGTCTTCCTACATGTCACGTATGTG
CCATCCCAGGAGAGGAACTTCACCACAGCGCCAGCAATTTGTCATGAAGGCAAAGCATACTTCCCTCGTG
AAGGTGTTTTTGTGTTTAATGGCACTTCTTGGTTTATTACACAGAGGAACTTCTTTTCTCCACAAATAAT
TACTACAGACAATACATTTGTCTCAGGAAATTGTGATGTCGTTATTGGCATCATTAACAACACAGTTTAT
GATCCTCTGCAACCTGAGCTCGACTCATTCAAAGAAGAGCTGGACAAGTACTTCAAAAATCATACATCAC
CAGATGTTGATCTTGGCGACATTTCAGGCATTAACGCTTCTGTCGTCAACATTCAAAAAGAAATTGACCG
CCTCAATGAGGTCGCTAAAAATTTAAATGAATCACTCATTGACCTTCAAGAATTGGGAAAATATGAGCAA
TATATTAAATGGCCTTGGTATGTTTGGCTCGGCTTCATTGCTGGACTAATTGCCATCGTCATGGTTACAA
TCTTGCTTTGTTGCATGACTAGTTGTTGCAGTTGCCTCAAGGGTGCATGCTCTTGTGGTTCTTGCTGCAA
GTTTGATGAGGATGACTCTGAGCCAGTTCTCAAGGGTGTCAAATTACATTACACATAA

FIG. 21

HR-C Native (SEQ ID NO:48).

1150	1161	1171	1181
DISGINASVVN	IQKEIDRLNE	VAKNLNESLI	DLQEL
ga d a d	a d	a d a	d

HR-C Analogue 1 (SEQ ID NO:67). Modulation of the "a" residue position

1150	1161	1171	1181
DISGINASVVN	IQKEIDRLNE	VIKNLNESLI	DLQEL

HR-C Analogue 2 (SEQ ID NO:68). Change of Helical propensity

1150	1161	1171	1181
DISGINASVVN	IQKEIARLNE	VAKALNESLI	DLQEL

HR-C Analogue 3 (SEQ ID NO:69). Change of Helical propensity and modulation of "a" position

1150	1161	1171	1181
DISGINASVVN	IQKEIARLNE	VIKALNESLI	DLQEL

HR-C Analogue 4 (SEQ ID NO:70). Change of Helical propensity

1150	1161	1171	1181
DIAAINASVAN	IQKEIARLNE	VAKALNESLA	ALQAL

HR-C Analogue 5 (SEQ ID NO:71). Introduction of lactam

1150	1161	1171	1181
DISGINASVVN	IQKEIERLNK	VAKNLNESLI	DLQEL
	[ ]		

HR-C Analogue 6 (SEQ ID NO:72). Introduction of salt bridge

1150	1161	1171	1181
DISGINASVVN	IQKEIERLNK	VAKNLNESLI	DLQEL

HR-C Analogue 7 (SEQ ID NO:73).

1150	1161	1171	1181
DIEEINKKVEE	IQKKIEELNK	KAEELNKKLE	ELQKK

HR-C Analogue 8 (SEQ ID NO:74). Introduction of salt bridges

1150	1161	1171	1181
DISGINASVVE	IQKKIEELNK	KAEELNKKLI	DLQEL

FIG. 22